RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/529,278_
Source: _PCT/10_
Date Processed by STIC: _12/20/05_

ENTERED

PCT

```
         RAW SEQUENCE LISTING                 DATE: 12/20/2005
         PATENT APPLICATION:  US/10/529,278   TIME: 10:29:11

         Input Set : A:\11582-010-999 Seqlist.txt
         Output Set: N:\CRF4\12202005\J529278.raw
```

```
 4 <110> APPLICANT: Inbe, Hisayo
 5         Encinas, Jeffrey
 7 <120> TITLE OF INVENTION: Regulation of Human P2Y15 G
 8         Protein-Coupled Receptor
10 <130> FILE REFERENCE: 11582-010-999
12 <140> CURRENT APPLICATION NUMBER: 10/529,278
13 <141> CURRENT FILING DATE: 2005-03-25
15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/010666
16 <151> PRIOR FILING DATE: 2003-09-25
18 <150> PRIOR APPLICATION NUMBER: 60/442,891
19 <151> PRIOR FILING DATE: 2003-01-28
21 <150> PRIOR APPLICATION NUMBER: 60/413,840
22 <151> PRIOR FILING DATE: 2002-09-27
24 <160> NUMBER OF SEQ ID NOS: 10
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1014
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo Sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)...(1014)
37 <400> SEQUENCE: 1
38 atg aat gag cca cta gac tat tta gca aat gct tct gat ttc ccc gat    48
39 Met Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe Pro Asp
40  1               5                  10                  15
42 tat gca gct gct ttt gga aat tgc act gat gaa aac atc cca ctc aag    96
43 Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys
44             20                  25                  30
46 atg cac tac ctc cct gtt att tat ggc att atc ttc ctc gtg gga ttt   144
47 Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe
48         35                  40                  45
50 cca ggc aat gca gta gtg ata tcc act tac att ttc aaa atg aga cct   192
51 Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
52      50                  55                  60
54 tgg aag agc agc acc atc att atg ctg aac ctg gcc tgc aca gat ctg   240
55 Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
56  65                  70                  75                  80
58 ctg tat ctg acc agc ctc ccc ttc ctg att cac tac tat gcc agt ggc   288
59 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
60                     85                  90                  95
62 gaa aac tgg atc ttt gga gat ttc atg tgt aag ttt atc cgc ttc agc   336
63 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser
```

```
64              100             105             110
66 ttc cat ttc aac ctg tat agc agc atc ctc ttc ctc acc tgt ttc agc   384
67 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
68         115             120             125
70 atc ttc cgc tac tgt gtg atc att cac cca atg agc tgc ttt tcc att   432
71 Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
72     130             135             140
74 cac aaa act cga tgt gca gtt gta gcc tgt gct gtg gtg tgg atc att   480
75 His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
76 145             150             155             160
78 tca ctg gta gct gtc att ccg atg acc ttc ttg atc aca tca acc aac   528
79 Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
80             165             170             175
82 agg acc aac aga tca gcc tgt ctc gac ctc acc agt tcg gat gaa ctc   576
83 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
84         180             185             190
86 aat act att aag tgg tac aac ctg att ttg act gca act act ttc tgc   624
87 Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
88         195             200             205
90 ctc ccc ttg gtg ata gtg aca ctt tgc tat acc acg att atc cac act   672
91 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr
92     210             215             220
94 ctg acc cat gga ctg caa act gac agc tgc ctt aag cag aaa gca cga   720
95 Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg
96 225             230             235             240
98 agg cta acc att ctg cta ctc ctt gca ttt tac gta tgt ttt tta ccc   768
99 Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro
100             245             250             255
102 ttc cat atc ttg agg gtc att cgg atc gaa tct cgc ctg ctt tca atc   816
103 Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
104             260             265             270
106 agt tgt tcc att gag aat cag atc cat gaa gct tac atc gtt tct aga   864
107 Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg
108         275             280             285
110 cca tta gct gct ctg aac acc ttt ggt aac ctg tta cta tat gtg gtg   912
111 Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
112     290             295             300
114 gtc agc gac aac ttt cag cag gct gtc tgc tca aca gtg aga tgc aaa   960
115 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys
116 305             310             315             320
118 gta agc ggg aac ctt gag caa gca aag aaa att agt tac tca aac aac   1008
119 Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn Asn
120             325             330             335
122 cct tga                                                           1014
123 Pro *
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 337
131 <212> TYPE: PRT
132 <213> ORGANISM: Homo Sapiens
```

```
134 <400> SEQUENCE: 2
135 Met Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe Pro Asp
136 1               5                   10                  15
137 Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys
138             20                  25                  30
139 Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe
140         35                  40                  45
141 Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
142     50                  55                  60
143 Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
144 65                  70                  75                  80
145 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
146             85                  90                  95
147 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser
148         100                 105                 110
149 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
150         115                 120                 125
151 Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
152     130                 135                 140
153 His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
154 145                 150                 155                 160
155 Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
156             165                 170                 175
157 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
158         180                 185                 190
159 Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
160         195                 200                 205
161 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr
162     210                 215                 220
163 Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg
164 225                 230                 235                 240
165 Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro
166             245                 250                 255
167 Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
168         260                 265                 270
169 Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg
170         275                 280                 285
171 Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
172     290                 295                 300
173 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys
174 305                 310                 315                 320
175 Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn Asn
176             325                 330                 335
177 Pro
180 <210> SEQ ID NO: 3
181 <211> LENGTH: 1014
182 <212> TYPE: DNA
183 <213> ORGANISM: Mus musculus
185 <220> FEATURE:
```

```
186 <221> NAME/KEY: CDS
187 <222> LOCATION: (1)...(1014)
189 <400> SEQUENCE: 3
190 atg att gag cca ctg gac agt cca gcc agt gat tcg gat ttc ctg gat   48
191 Met Ile Glu Pro Leu Asp Ser Pro Ala Ser Asp Ser Asp Phe Leu Asp
192 1               5                   10                  15
194 tac cca agt gct ctg gga aac tgc acc gac gag caa atc tca ttc aag   96
195 Tyr Pro Ser Ala Leu Gly Asn Cys Thr Asp Glu Gln Ile Ser Phe Lys
196                 20                  25                  30
198 atg cag tac ctt ccc gtc atc tat agc atc atc ttc ctc gtg ggc ttc  144
199 Met Gln Tyr Leu Pro Val Ile Tyr Ser Ile Ile Phe Leu Val Gly Phe
200             35                  40                  45
202 ccg ggg aac aca gtg gcc atc tcc atc tac att ttc aag atg cgg ccg  192
203 Pro Gly Asn Thr Val Ala Ile Ser Ile Tyr Ile Phe Lys Met Arg Pro
204     50                  55                  60
206 tgg agg ggc agt aca gtc atc atg ctg aac ctg gcc ttg acg gac ttg  240
207 Trp Arg Gly Ser Thr Val Ile Met Leu Asn Leu Ala Leu Thr Asp Leu
208 65                  70                  75                  80
210 ctg tat ctg acc agc ctc ccg ttc ctc atc cat tac tat gcc agt ggt  288
211 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
212                 85                  90                  95
214 gaa aac tgg atc ttt gga gat ttc atg tgc aag ttc atc cgc ttc ggc  336
215 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly
216                 100                 105                 110
218 ttc cac ttc aac ctc tac agc agc att ctc ttc ctc acc tgc ttc agt  384
219 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
220             115                 120                 125
222 ctc ttc cgt tac gtt gtg atc att cac ccg atg agc tgc ttt tct att  432
223 Leu Phe Arg Tyr Val Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
224     130                 135                 140
226 cag aaa act cgc tgg gca gtg gta gct tgt gcc ggg gtg tgg gtc att  480
227 Gln Lys Thr Arg Trp Ala Val Val Ala Cys Ala Gly Val Trp Val Ile
228 145                 150                 155                 160
230 tct ttg gta gct gtc atg ccc atg act ttc ctg atc aca tca acc acc  528
231 Ser Leu Val Ala Val Met Pro Met Thr Phe Leu Ile Thr Ser Thr Thr
232                 165                 170                 175
234 cgg acc aat agg tct gct tgc ctt gac ctc acc agt tca gat gac ctc  576
235 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Asp Leu
236             180                 185                 190
238 act act atc aag tgg tac aat ctc att ttg aca gcc acc act ttc tgc  624
239 Thr Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
240             195                 200                 205
242 ctg cca ttg gtg ata gtg aca ctt tgc tac acg aca att atc agt acc  672
243 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile Ser Thr
244     210                 215                 220
246 ctg act cac ggg cct cgg acc cac agc tgc ttt aag cag aag gct cgg  720
247 Leu Thr His Gly Pro Arg Thr His Ser Cys Phe Lys Gln Lys Ala Arg
248 225                 230                 235                 240
250 aga ctg act att ctg ctc ctc ctt gtt ttc tat ata tgt ttc tta ccc  768
```

```
251 Arg Leu Thr Ile Leu Leu Leu Leu Val Phe Tyr Ile Cys Phe Leu Pro
252              245             250             255
254 ttc cac atc ttg agg gtc att cgg atc gaa tct cgc ctg ctt tca atc    816
255 Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
256              260             265             270
258 agc tgc tcc atc gag agt cac atc cac gaa gct tac att gtt tct aga    864
259 Ser Cys Ser Ile Glu Ser His Ile His Glu Ala Tyr Ile Val Ser Arg
260          275             280             285
262 cca tta gct gct ctc aac acc ttt ggc aac ctg ctg tta tat gtt gtg    912
263 Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
264      290             295             300
266 gtc agc aat aac ttc cag cag gca ttc tgc tct ata gtg aga tgc aaa    960
267 Val Ser Asn Asn Phe Gln Gln Ala Phe Cys Ser Ile Val Arg Cys Lys
268 305             310             315             320
270 gcc agt ggg gac ctt gaa caa gga aag aaa gac agt tgc tca aac aac   1008
271 Ala Ser Gly Asp Leu Glu Gln Gly Lys Lys Asp Ser Cys Ser Asn Asn
272              325             330             335
274 cct tga                                                          1014
275 Pro *
279 <210> SEQ ID NO: 4
280 <211> LENGTH: 337
281 <212> TYPE: PRT
282 <213> ORGANISM: Mus musculus
284 <400> SEQUENCE: 4
285 Met Ile Glu Pro Leu Asp Ser Pro Ala Ser Asp Ser Asp Phe Leu Asp
286 1             5               10              15
287 Tyr Pro Ser Ala Leu Gly Asn Cys Thr Asp Glu Gln Ile Ser Phe Lys
288              20              25              30
289 Met Gln Tyr Leu Pro Val Ile Tyr Ser Ile Ile Phe Leu Val Gly Phe
290          35              40              45
291 Pro Gly Asn Thr Val Ala Ile Ser Ile Tyr Ile Phe Lys Met Arg Pro
292      50              55              60
293 Trp Arg Gly Ser Thr Val Ile Met Leu Asn Leu Ala Leu Thr Asp Leu
294 65              70              75              80
295 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
296              85              90              95
297 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly
298          100             105             110
299 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
300          115             120             125
301 Leu Phe Arg Tyr Val Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
302      130             135             140
303 Gln Lys Thr Arg Trp Ala Val Val Ala Cys Ala Gly Val Trp Val Ile
304 145             150             155             160
305 Ser Leu Val Ala Val Met Pro Met Thr Phe Leu Ile Thr Ser Thr Thr
306              165             170             175
307 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Asp Leu
308          180             185             190
309 Thr Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
```

VERIFICATION SUMMARY   DATE: 12/20/2005
PATENT APPLICATION: **US/10/529,278**   TIME: 10:29:12

Input Set : **A:\11582-010-999 Seqlist.txt**
Output Set: **N:\CRF4\12202005\J529278.raw**